

F. Hamud

1646

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/202,455

DATE: 01/19/2000
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This Raw Listing contains the General Information
Section and up to first 5 pages.

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1 <110> APPLICANT: Yamaguchi, Kyoji
2 Yasuda, Hisataka
3 Nakagawa, Nobuaki
4 Shima, Nobuyuki
5 Kinoshita, Masahiko
6 Tsuda, Eisuke
7 Goto, Masaaki
8 Yano, Kazuki
9 Tomoyasu, Akihiro
10 Kobayashi, Fumie
11 Washida, Naohiro
12 Takahashi, Ken
13 Morinaga, Tomonori
14 Higashio, Kanji
15 <120> TITLE OF INVENTION: Novel Protein and Method for Producing the Protein
16 <130> FILE REFERENCE: FJN-070
17 <140> CURRENT APPLICATION NUMBER: US/09/202,455
18 <141> CURRENT FILING DATE: 1998-12-15
19 <150> EARLIER APPLICATION NUMBER: JP 97808/1997
20 <151> EARLIER FILING DATE: 1997-04-15
21 <150> EARLIER APPLICATION NUMBER: JP 151434/1997
22 <151> EARLIER FILING DATE: 1997-06-09
23 <150> EARLIER APPLICATION NUMBER: JP 217897/1997
24 <151> EARLIER FILING DATE: 1997-08-12
25 <150> EARLIER APPLICATION NUMBER: JP 224803/1997
26 <151> EARLIER FILING DATE: 1997-08-21
27 <150> EARLIER APPLICATION NUMBER: JP 332241/1997
28 <151> EARLIER FILING DATE: 1997-12-02
29 <150> EARLIER APPLICATION NUMBER: WO PCT/JP98/01728
30 <151> EARLIER FILING DATE: 1998-04-15
31 <160> NUMBER OF SEQ ID NOS: 19
32 <170> SOFTWARE: PatentIn Ver. 2.0
33 <210> SEQ ID NO 1
34 <211> LENGTH: 316
35 <212> TYPE: PRT
36 <213> ORGANISM: Mus musculus
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41 20 25 30
42 Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Ala Ala Ser Arg Ser
43 35 40 45
44 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser

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49          85          90          95
50   Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
51          100          105          110
52   Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
53          115          120          125
54   Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
55          130          135          140
56   Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
57          145          150          155          160
58   Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
59          165          170          175
60   Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
61          180          185          190
62   Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
63          195          200          205
64   Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
65          210          215          220
66   Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
67          225          230          235          240
68   Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
69          245          250          255
70   Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
71          260          265          270
72   Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
73          275          280          285
74   Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
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85   cgccatgcgc cgggccagcc gagactacgg caagtacctg cgcagctcgg aggagatggg 180
86   cagcggcccc ggcgtccac acgaggggtcc gctgcacccc gcgccttctg caccggctcc 240
87   ggcgcgcgca ccgcgcgct ccgcgtccat gttcctggcc ctctggggc tgggactggg 300
88   ccaggtggtc tgcagcatcg ctctgttctt gtactttcga gcgcagatgg atcctaacag 360
89   aatatcagaa gacagcactc actgctttta tagaatcctg agactccatg aaaacgcagg 420
90   tttgcaggac tcgactcttg agagtgaaga cacactacct gactcctgca ggaggatgaa 480
91   acaagccttt cagggggccg tgcagaagga actgcaacac attgtggggc cacagcgctt 540
92   ctcaggagct ccagctatga tggaaggctc atggttgat gtggcccagc gaggcaagcc 600
93   tgaggcccag ccatttgac acctcaccat caatgctgcc agcatcccat cgggttccca 660
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97      gtatgtcggt aaaaccagca tcaaaatccc aagttctcat aacctgatga aaggagggag 900
98      cacgaaaaac tggtcgggca attctgaatt ccacttttat tccataaatg ttgggggatt 960
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102     atgtctatac atgtgtaaga ctactaagag acatggcca cgggtgatga aactcacagc 1200
103     cctctctctt gagcctgtac aggttggtga tatgtaaagt ccataggtga tgtagattc 1260
104     atggtgatta cacaacggtt ttacaatttt gtaatgattt ctagaattg aaccagattg 1320
105     ggagaggtat tccgatgctt atgaaaaact tacacgtgag ctatggaagg gggtcacagt 1380
106     ctctgggtct aaccctgga catgtgccac tgagaacctt gaaattaaga ggatgccatg 1440
107     tcattgcaaa gaaatgatag tgtgaagggt taagtctctt tgaattgtta cattgctgctg 1500
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114 <223> OTHER INFORMATION: Description of Artificial Sequence:primer

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119 <212> TYPE: DNA

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122 <223> OTHER INFORMATION: Description of Artificial Sequence:primer

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128 <213> ORGANISM: Artificial Sequence

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130 <223> OTHER INFORMATION: Description of Artificial Sequence:primer

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136 <213> ORGANISM: Artificial Sequence

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142 <211> LENGTH: 26

143 <212> TYPE: DNA

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153 <220> FEATURE:
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158 <211> LENGTH: 20
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160 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
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167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial Sequence
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182     Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
183         35             40             45
184     Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
185         50             55             60
186     Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
187         65             70             75             80
188     Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
189         85             90             95
190     Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
191         100            105            110
192     Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
193         115            120            125
194     Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys

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199          165          170          175
200 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
201          180          185          190
202 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
203          195          200          205
204 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
205          210          215          220
206 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
207          225          230          235          240
208 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
209          245          250          255
210 Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
211          260          265          270
212 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
213          275          280          285
214 Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
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225 cccctgcgcg cctccgcgc catgttcgtg gccctcctgg ggctggggct gggccagggt 180
226 gtctgcagcg tcgccctgtt cttctatttc agagcgcaga tggatcctaa tagaatatca 240
227 gaagatggca ctactgcat ttatagaatt ttgagactcc atgaaaatgc agattttcaa 300
228 gacacaactc tggagagtca agatacaaaa ttaatactg attcatgtag gagaattaaa 360
229 caggcctttc aaggagctgt gcaaaaggaa ttacaacata tcgttggatc acagcacatc 420
230 agagcagaga aagcgatggt ggatggctca tggttagatc tggccaagag gagcaagctt 480
231 gaagctcagc cttttgctca tctactatt aatgccaccg acatcccatc tggttcccat 540
232 aaagtgagtc tgtcctcttg gtaccatgat cgggggttggg ccaagatctc caacatgact 600
233 tttagcaatg gaaaactaat agttaatcag gatggcctttt attacctgta tgccaacatt 660
234 tgctttcgac atcatgaaac ttcaggagac ctactacag agtatcttca actaatggtg 720
235 tacgtcacta aaaccagcat caaatccca agttctcata ccctgatgaa aggaggaagc 780
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243 <220> FEATURE:
244 <223> OTHER INFORMATION: Description of Artificial Sequence:human OBM SF

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